# Predicting meat quality with biomarkers

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In the course of the EU QPorkChains project, biomarkers have been tested as a tool for monitoring meat traits

**The EU funded project Quality Pork Chains (QPorkChains) (2007-2012) aimed at improving pork production chains for higher quality. Part of the project was to develop biomarkers using new genomics technologies, which can further be translated to tools in order to monitor and predict pork quality. Such tools will enable usage of the variation in meat quality at the level of breeding and at the slaughterhouses. The project aimed at developing innovative knowledge and tools for the pork production industries to improve their economics. Here results are summarised regarding the identification and validation of biomarkers – what can the industry do with biomarkers, and where are we at this moment?**

**By Marinus F.W. te Pas, Bénédicte Lebret, Marie Damon, Bo Thomsen, Mariusz Pierzchala, Agnieszka Korwin-Kossakowska, Kui Li, Lars Kristensen, Jette F. Young, Birthe Pedersen and Niels Oksbjerg**

Biological processes determine livestock production traits and the final meat quality traits. These biological processes are genetically determined and modulated by interactions with the environment of the animals. Such interactions with the environment may include feeding regimes, nutrient content of feeds, rearing conditions including ambient temperature, housing system, stress factors, etc. For traits related to meat quality, the heritability is generally low (typically 10–25%, probably with an exception for meat redness and intramuscular fat showing higher heritability) making the interactions with the environment more important. Thus, genetic (DNA) markers have limited value for such traits. Biomarkers of genome expression (later called "biomarkers" in the text) by considering the genes actually expressed in a specific tissue and a specific physiological condition, can measure the net effect of the genetics and the interactions with the environment, and are therefore most useful for traits related to meat quality. Biomarkers (Fig. 1) thus result from both genetics and the environmental impact on genome expression.

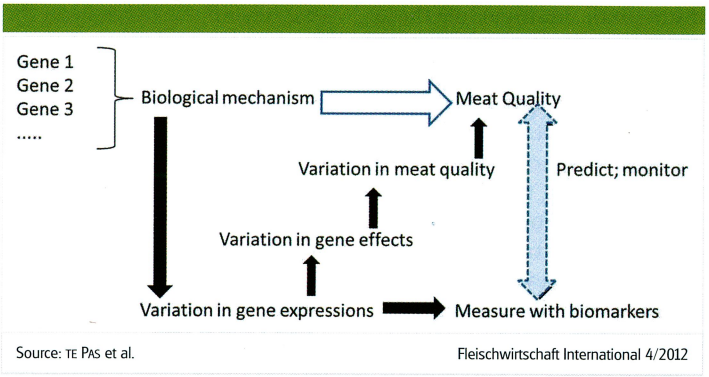



Fig. 1: Mode of operation of biomarkers

Genes are expressed in tissues, and work together in biological mechanisms in vivo as well as in conversion of muscle to meat. Variations in gene expression regulate biological mechanisms and are therefore associated to variation in meat quality. This variation in gene expression can be measured with biomarkers, which can be used to monitor and predict the meat quality.

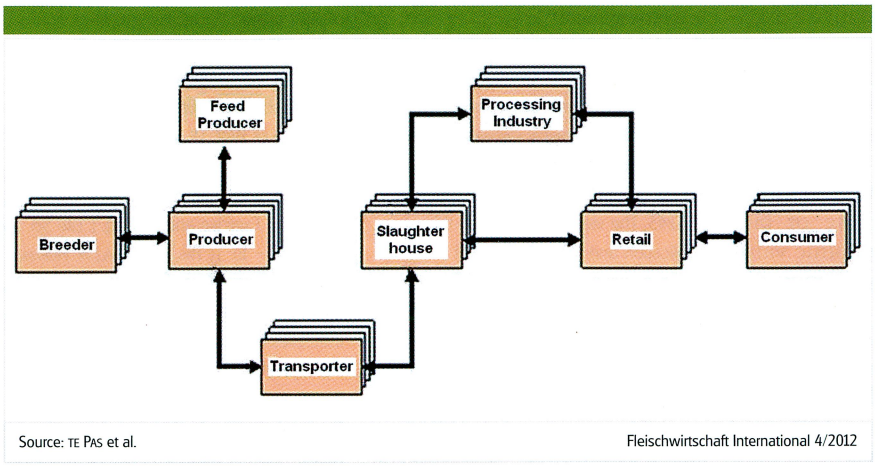
Current investigations aiming to elucidate the biological mechanisms underlying economically important livestock traits often include omics technologies, i.e. technologies based upon knowledge of the genome sequence of the animal species. Today the genome sequences of most livestock species have been elucidated. Knowing the biological background of traits enables identification of relevant processes, genes or molecules that may be used as indicators to rapidly and easy detect the status and phase of biological processes. Such indicators are called biomarkers. Thus biomarkers provide information about the status and phase of biological processes underlying particular traits. This information can be used to optimise the economic value of these traits. Thus, the industries can use biomarkers to optimise the economic values of the pork production chains. This project developed biomarkers to be used at the stage of slaughter.

## Biomarkers for the pork production chain

In the QPorkChains programme, biomarkers were discovered using pork samples from European commercial chains in Germany, Spain, and Poland, and experimental chains in France. A further study was done by the colleagues from P.R. China using a Chinese experimental pork production chain. In Denmark and The Netherlands an additional experiment was done to discover biomarkers for transport stress, using exercise as a model, in relation to meat quality. Biomarker discovery studies were

done at the levels of gene expression and protein expression. The discovered biomarkers were confirmed in the same animal samples as for their identification, using a different methodology.

Afterwards, the more 'robust' biomarkers in terms of correlation with meat quality traits were used for validation in a different and independent set of samples as for identification. Thus, validation was undertaken on experimental pork chains of same and of different genotypes as for identification (France), and on commercial pork chains, including a Danish commercial set of 100 samples specifically phenotyped for meat quality traits. This is to ensure that the biomarkers will also be useful for other pork chains than the ones studied in the project. Meat quality for all samples was determined with standard technological parameters. Organoleptic data were obtained for the France experimental pork chains using a test panel. Table 1 shows the numbers of biomarkers obtained for all meat quality traits. Most of these biomarkers are expression levels of genes. For $pH_{24}$ and drip loss, also protein associations are shown. Biomarkers showing the relation between transport stress, lairage waiting time, and meat quality traits are not included in the table. These biomarkers were only characterised as anonymous markers. While such biomarkers can be used by the industry, they are of different nature and require specific expertise different from the ones in the table. The present status of the biomarkers is that biomarker tests are available for use in commercial applications, but the tests do require specific expertise to perform an interpretation of the results. Moreover, the results show that a combination of markers instead of a single one should be considered to determine the level of a given meat quality trait in pork samples. It is therefore recommended that interested industries should contact the authors for commercial application of the biomarkers.




Source: TE PAS et al. Fleischwirtschaft International 4/2012

**Fig. 2:** The industries of the pork production chain

## How can the pork production industries use biomarkers

A typical pork production chain (Fig. 2) consists of different industries including the breeder, producer (probably with a multiplier in between) and their relationship with the feed producer. When the pigs are at slaughter weight the transporter brings them to the slaughterhouse, and the carcasses are transported to the retail either directly or via the processing industry. The consumer is the endpoint of the chain. Because the impact of genetic makeup is low to moderate on meat quality, environmental influences such as the rearing conditions of the pigs, their pre-slaughter handling, as well as the processing conditions of carcasses and pork products largely in-

## Combination of markers should be considered

**Tab.:** Number of detected and validated biomarkers

| Trait | No. detected Biomarkers | No. validated Biomarkers |
|---|---|---|
| $pH_{24}$ | 16 (19) | 8 |
| IMF | 8 | 6 |
| Drip loss | 23 (21) | 15 |
| Juiciness | 6 | 2 |
| Tenderness | 3 | 2 |
| Shear force | 4 | 3 |
| **Meat colour** | | |
| a* | 20 | 7 |
| b* | 8 | 3 |
| C* | 10 | 0 |
| L* | 14 | 6 |
| Reflection | 4 | 0 |
| $H^0$ | 8 | 5 |

$pH_{24}$: pH in the meat 24 hours after slaughtering the pig, usually measured at the last rib curvature in the *longissimus* muscle; IMF: Intra muscular fat; not visible fat in meat; a*: Measure of the redness of the loin muscle (on a green – red axis); b*: Measure of the yellowness of the loin muscle (on a blue – yellow axis); C*: Calculated root of the sum of the squares of a* and b*; The data indicate the colour saturation; L*: Lightness of loin muscle; $H^0$: Calculated from a* and b*; The data indicate the hue of the meat between red (0°) and yellow (90°).

Only the most robust biomarkers showing highest correlations with meat quality traits were validated. Numbers within parenthesis are protein biomarkers.

Source: TE PAS et al. Fleischwirtschaft International 4/2012

fluence the meat quality experienced by the consumers. Thus, producing higher quality pork requires the combined action of all industries. In a recent review it was shown that all industries in the pork production chain can benefit from the use of biomarkers as the economic value can be increased for all industries. A coordinated action of all industries in the pork production chain can increase the economic profit of all.

The biomarkers could be used for two applications:

- to monitor meat quality traits, and better define them for clients and consumers
- to predict the outcome of actions taken to improve the meat quality, and thereby regulate meat quality improving actions.

## Conclusion

The project provided a proof of principle showing that biomarkers can be used to monitor and predict pork quality but also indicates that up to 5–10 biomarkers in combination may be needed to obtain an acceptable prediction of a given meat quality trait. For most technical meat quality traits biomarkers are available and validated.

The biomarkers were developed and further validated in a number of both experimental and commercial pork production chains showing that they can be used by the diverse industries in a variety of pork production chains.



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Purac

# Effectively watching out for *Listeria*

Purac with its headquarter in Gorinchem, The Netherlands, claims that the new web version of its *Listeria* control software can reduce food product development time by two to three months, saving costs as well as indicating the presence of any harmful pathogens. According to EU legislation, *L. monocytogenes* must not be present in levels above 100 cfu/g during shelf life. The predictive *Listeria* Control Model was designed to accelerate time-to-market by cutting the cost and duration of R&D. For a product with a 50-day shelf life, the manufacturer will normally carry out three shelf life tests over a period of nine or 10 months. This tool shortens development time to five to six months, an average reduction of two or three months. To test for pathogens, manufacturers describe the food product by entering parameters such as salt content, as well as the storage temperature and moisture content.

The software uses the data to generate a "best fit" line by connecting the most probable *Listeria* counts for every point in time to predict *Listeria* growth for the specific food characteristics. By taking into account variations between food product batches, the technology simulates "worst case scenarios" where *Listeria* growth is highest. The fatality of *Listeria* poisoning is very high; there is a 25–30% chance of death. It is especially dangerous to the elderly and pregnant women.The online aspect of the software is important because users always have access to the latest technology. The software is available on the website.

**www.purac.com**


The *Listeria* control software can reduce the new-product-develop time.